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High Throughput Optimization of Initial Crystallization Conditions. J.R. Luft^{1, 2}, S.M. Gulde¹, A.M. Lauricella¹, M.I. Said¹, J.L. Smith¹, M. Thayer¹, C.K. Veatch¹, J.R. Wolfley¹, M.G. Malkowski^{1, 2}, G.T. DeTitta^{1, 2}, ¹The Hauptman Woodward Medical Research Inst., ²Dept. of Structural Biology, SUNY at Buffalo, 700 Ellicott St., Buffalo, New York 14203.

An established High Throughput infrastructure screens 200 biological macromolecules against 1536 chemical conditions each month to determine initial chemical crystallization conditions (1). The majority of these samples are provided by structural biologists with a subset of difficult to crystallize targets from *Saccharomyces cerevisiae* supplied by the CHTSB consortia. High Throughput optimization methods are under development to use information obtained from the screening experiments to produce crystals of sufficient size and quality for X-ray diffraction. First phase optimization trials use a simple volumetric approach to refine crystallization conditions in the experiment drop (2). This method was applied to 17 samples from the structural biology community set up in replicate 1536 well plates, incubated at four different temperatures. The outcomes of these experiments and other optimization methods that are under investigation will be described. This work is supported in part by NIH U54 GM074899-01.

1) *Journal of Structural Biology* **142**, 170-179 (2003)

2) *Structure* **10** (2) 147-151 (2002)